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U.S. APPLICATION NUMBER NO.	FIRST NAMED APPLICANT	ATTY. DOCKET NO.
10/566,944	Thorsten Zank	12810-00193-US

INTERNATIONAL APPLICATION NO.

PCT/EP04/07957

I.A. FILING DATE

07/16/2004

PRIORITY DATE

08/01/2003

23416
 CONNOLLY BOVE LODGE & HUTZ, LLP
 P O BOX 2207
 WILMINGTON, DE 19899

CONFIRMATION NO. 5346

371 FORMALITIES LETTER



OC000000023991140

Date Mailed: 05/22/2007

NOTIFICATION TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

Applicant is cautioned that correction of the above items may cause the specification and drawings page count to exceed 100 pages. If the specification and drawings exceed 100 pages, applicant will need to submit the required application size fee.

For questions regarding compliance to 37 CFR 1.821-1.825 requirements, please contact:

- For Rules Interpretation, call (571) 272-0951
- For Patent Software Program Help, call Patent EBC at 1-866-217-9197 or directly at 703-305-3028 / 703-308-6845 between the hours of 6 a.m. and 12 midnight, Monday through Friday, EST.
- Send e-mail correspondence for Patent Software Program Help @ ebc@uspto.gov

Applicant is reminded that any communications to the United States Patent and Trademark Office must be mailed to the address given in the heading and include the U.S. application no. shown above (37 CFR 1.5)

Registered users of EFS-Web may alternatively submit their reply to this notice via EFS-Web.
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For more information about EFS-Web please call the USPTO Electronic Business Center at 1-866-217-9197 or visit our website at <http://www.uspto.gov/ebc>.

If you are not using EFS-Web to submit your reply, you must include a copy of this notice.

KAREN R MCLEAN

Telephone: (703) 308-9140 EXT 214

PART 1 - ATTORNEY/APPLICANT COPY

U.S. APPLICATION NUMBER NO.	INTERNATIONAL APPLICATION NO.	ATTY. DOCKET NO.
10/566,944	PCT/EP04/07957	12810-00193-US

FORM PCT/DO/EO/922 (371 Formalities Notice)

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____

Source: _____

Date Processed by STIC: _____

10/566,944
JFWP
02/14/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/cbknote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

SUGGESTED CORRECTION

SERIAL NUMBER:

10/566,944

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|--|--|
| 1 | Wrapped Nucleic
Amino Acids | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." |
| 2 | Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. |
| 3 | Misaligned Amino
Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. |
| 4 | Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. |
| 5 | Variable Length | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. |
| 6 | PatentIn 2.0
"bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 7 | Skipped Sequences
(OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |
| 8 | Skipped Sequences
(NEW RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 9 | Use of n's or Xaa's
(NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
<u>Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.</u>
<u>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.</u> |
| 10 | Invalid <213>
Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence |
| 11 | Use of <220> | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) |
| 12 | PatentIn 2.0
"bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. |
| 13 | Misuse of n/Xaa | "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid |



IFWP

RAW SEQUENCE LISTING

DATE: 02/14/2006

PATENT APPLICATION: US/10/566,944

TIME: 12:55:17

Input Set : F:\Sequence listing (12810-00193-US).txt

Output Set: N:\CRF4\02142006\J566944.raw

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3 <110> APPLICANT: Zank, Thorsten
4      Bauer, Jorg
5      Cirpus, Petra
6      Abbadi, Amine
7      Heinz, Ernst
8      Qiu, Xiao
9      Vrinten, Patricia
10     Sperling, Petra
11     Domergue, Frederic
12     Meyer, Astrid
13     Kirsch, Jelena
15 <120> TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF MULTIPLE-UNSATURATED FATTY
ACIDS IN
16     TRANSGENIC ORGANISMS
18 <130> FILE REFERENCE: 12810-00193-US
!--> 20 <140> CURRENT APPLICATION NUMBER: US/10/566,944
!--> 20 <141> CURRENT FILING DATE: 2006-02-01
20 <150> PRIOR APPLICATION NUMBER: DE 103 35 992.3
21 <151> PRIOR FILING DATE: 2003-08-01
23 <150> PRIOR APPLICATION NUMBER: DE 103 44 557.9
24 <151> PRIOR FILING DATE: 2003-09-24
26 <150> PRIOR APPLICATION NUMBER: DE 103 47 869.8
27 <151> PRIOR FILING DATE: 2003-10-10
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30 <151> PRIOR FILING DATE: 2003-12-18
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33 <151> PRIOR FILING DATE: 2004-02-27
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36 <151> PRIOR FILING DATE: 2004-03-13
38 <150> PRIOR APPLICATION NUMBER: DE 10 2004 024 014.0
39 <151> PRIOR FILING DATE: 2004-05-14
41 <160> NUMBER OF SEQ ID NOS: 192
43 <170> SOFTWARE: PatentIn version 3.1
46 <210> SEQ ID NO: 1
47 <211> LENGTH: 1266
48 <212> TYPE: DNA
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48

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Input Set : F:\Sequence listing (12810-00193-US).txt

Output Set: N:\CRF4\02142006\J566944.raw

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62 Tyr Asp Val Ser Ala Trp Val Asn Phe His Pro Gly Gly Ala Glu Ile
63          20          25          30
65 ata gag aat tac caa gga agg gat gcc act gat gcc ttc atg gtt atg      144
66 Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
68          35          40          45
70 cac tct caa gaa gcc ttc gac aag ctc aag cgc atg ccc aaa atc aat      192
71 His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
72          50          55          60
74 ccc agt tct gag ttg cca ccc cag gct gca gtg aat gaa gct caa gag      240
75 Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
76 65          70          75          80
78 gat ttc cgg aag ctc cga gaa gag ttg atc gca act ggc atg ttt gat      288
79 Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
80          85          90          95
82 gcc tcc ccc ctc tgg tac tca tac aaa atc agc acc aca ctg ggc ctt      336
83 Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
84          100          105          110
86 gga gtg ctg ggt tat ttc ctg atg gtt cag tat cag atg tat ttc att      384
87 Gly Val Leu Gly Tyr Phe Leu Met Val Gln Tyr Gln Met Tyr Phe Ile
88          115          120          125
90 ggg gca gtg ttg ctt ggg atg cac tat caa cag atg ggc tgg ctt tct      432
91 Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
92          130          135          140
94 cat gac att tgc cac cac cag act ttc aag aac cgg aac tgg aac aac      480
95 His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
96 145          150          155          160
98 ctc gtg gga ctg gta ttt ggc aat ggt ctg caa ggt ttt tcc gtg aca      528
99 Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
101          165          170          175
103 tgc tgg aag gac aga cac aat gca cat cat tcg gca acc aat gtt caa      576
104 Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
105          180          185          190
107 ggg cac gac cct gat att gac aac ctc ccc ctc tta gcc tgg tct gag      624
108 Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
109          195          200          205
111 gat gac gtc aca cgg gcg tca ccg att tcc cgc aag ctc att cag ttc      672
112 Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
113          210          215          220
115 cag cag tat tat ttc ttg gtc atc tgt atc ttg ttg cgg ttc att tgg      720
116 Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
117 225          230          235          240
119 tgt ttc cag agc gtg ttg acc gtg cgc agt ctg aag gac aga gat aac      768
120 Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
121          245          250          255
123 caa ttc tat cgc tct cag tat aag aag gag gcc att ggc ctc gcc ctg      816
124 Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
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DATE: 02/14/2006

PATENT APPLICATION: US/10/566,944

TIME: 12:55:17

Input Set : F:\Sequence listing (12810-00193-US).txt

Output Set: N:\CRF4\02142006\J566944.raw

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131 ctc aca tcg ctg ttg gta ttt ttc gtt tcg gag ctg gtt ggc ggc ttc      912
132 Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
135      290      295      300
137 ggc att gcg atc gtg gtg ttc atg aac cac tac cca ctg gag aag atc      960
138 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
139 305      310      315      320
141 ggg gac tcg gtc tgg gat ggc cat gga ttc tcg gtt ggc cag atc cat      1008
142 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
143      325      330      335
145 gag acc atg aac att cgg cga ggg att atc aca gat tgg ttt ttc gga      1056
146 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
147      340      345      350
149 ggc ttg aac tac cag atc gag cac cat ttg tgg ccg acc ctc cct cgc      1104
150 Gly Leu Asn Tyr Gln Ile Glu His His Leu Trp Pro Thr Leu Pro Arg
151      355      360      365
153 cac aac ctg aca gcg gtt agc tac cag gtg gaa cag ctg tgc cag aag      1152
154 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
155      370      375      380
157 cac aac ctg ccg tat cgg aac ccg ctg ccc cat gaa ggg ttg gtc atc      1200
158 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
159 385      390      395      400
161 ctg ctg cgc tat ctg gcg gtg ttc gcc cgg atg gcg gag aag caa ccc      1248
162 Leu Leu Arg Tyr Leu Ala Val Phe Ala Arg Met Ala Glu Lys Gln Pro
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168      420
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172 <211> LENGTH: 421
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174 <213> ORGANISM: Euglena gracilis
176 <400> SEQUENCE: 2
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183      20      25      30
186 Ile Glu Asn Tyr Gln Gly Arg Asp Ala Thr Asp Ala Phe Met Val Met
187      35      40      45
190 His Ser Gln Glu Ala Phe Asp Lys Leu Lys Arg Met Pro Lys Ile Asn
191      50      55      60
194 Pro Ser Ser Glu Leu Pro Pro Gln Ala Ala Val Asn Glu Ala Gln Glu
195 65      70      75      80
198 Asp Phe Arg Lys Leu Arg Glu Glu Leu Ile Ala Thr Gly Met Phe Asp
199      85      90      95
202 Ala Ser Pro Leu Trp Tyr Ser Tyr Lys Ile Ser Thr Thr Leu Gly Leu
203      100      105      110

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DATE: 02/14/2006

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Output Set: N:\CRF4\02142006\J566944.raw

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207      115      120      125
210 Gly Ala Val Leu Leu Gly Met His Tyr Gln Gln Met Gly Trp Leu Ser
211      130      135      140
214 His Asp Ile Cys His His Gln Thr Phe Lys Asn Arg Asn Trp Asn Asn
215 145      150      155      160
218 Leu Val Gly Leu Val Phe Gly Asn Gly Leu Gln Gly Phe Ser Val Thr
219      165      170      175
222 Cys Trp Lys Asp Arg His Asn Ala His His Ser Ala Thr Asn Val Gln
223      180      185      190
226 Gly His Asp Pro Asp Ile Asp Asn Leu Pro Leu Leu Ala Trp Ser Glu
227      195      200      205
230 Asp Asp Val Thr Arg Ala Ser Pro Ile Ser Arg Lys Leu Ile Gln Phe
231      210      215      220
234 Gln Gln Tyr Tyr Phe Leu Val Ile Cys Ile Leu Leu Arg Phe Ile Trp
235 225      230      235      240
238 Cys Phe Gln Ser Val Leu Thr Val Arg Ser Leu Lys Asp Arg Asp Asn
239      245      250      255
242 Gln Phe Tyr Arg Ser Gln Tyr Lys Lys Glu Ala Ile Gly Leu Ala Leu
243      260      265      270
246 His Trp Thr Leu Lys Ala Leu Phe His Leu Phe Phe Met Pro Ser Ile
247      275      280      285
250 Leu Thr Ser Leu Leu Val Phe Phe Val Ser Glu Leu Val Gly Gly Phe
251      290      295      300
254 Gly Ile Ala Ile Val Val Phe Met Asn His Tyr Pro Leu Glu Lys Ile
255 305      310      315      320
258 Gly Asp Ser Val Trp Asp Gly His Gly Phe Ser Val Gly Gln Ile His
259      325      330      335
262 Glu Thr Met Asn Ile Arg Arg Gly Ile Ile Thr Asp Trp Phe Phe Gly
263      340      345      350
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267      355      360      365
270 His Asn Leu Thr Ala Val Ser Tyr Gln Val Glu Gln Leu Cys Gln Lys
271      370      375      380
274 His Asn Leu Pro Tyr Arg Asn Pro Leu Pro His Glu Gly Leu Val Ile
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293 <222> LOCATION: (1)..(777)
294 <223> OTHER INFORMATION: delta9-elongase
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DATE: 02/14/2006

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Output Set: N:\CRF4\02142006\J566944.raw

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299	1			5					10					15			
301	gac	ccg	gaa	atc	ctc	att	ggc	acc	ttc	tcg	tac	ttg	cta	ctc	aaa	ccg	96
302	Asp	Pro	Glu	Ile	Leu	Ile	Gly	Thr	Phe	Ser	Tyr	Leu	Leu	Leu	Lys	Pro	
303				20					25					30			
305	ctg	ctc	cgc	aat	tcc	ggg	ctg	gtg	gat	gag	aag	aag	ggc	gca	tac	agg	144
306	Leu	Leu	Arg	Asn	Ser	Gly	Leu	Val	Asp	Glu	Lys	Lys	Gly	Ala	Tyr	Arg	
307				35					40					45			
309	acg	tcc	atg	atc	tgg	tac	aac	gtt	ctg	ctg	gcg	ctc	ttc	tct	gcg	ctg	192
310	Thr	Ser	Met	Ile	Trp	Tyr	Asn	Val	Leu	Leu	Ala	Leu	Phe	Ser	Ala	Leu	
311				50					55					60			
313	agc	ttc	tac	gtg	acg	gcg	acc	gcc	ctc	ggc	tgg	gac	tat	ggg	acg	ggc	240
314	Ser	Phe	Tyr	Val	Thr	Ala	Thr	Ala	Leu	Gly	Trp	Asp	Tyr	Gly	Thr	Gly	
315	65								70					75			80
317	gcg	tgg	ctg	cgc	agg	caa	acc	ggc	gac	aca	ccg	cag	ccg	ctc	ttc	cag	288
318	Ala	Trp	Leu	Arg	Gln	Thr	Gly	Asp	Thr	Pro	Gln	Pro	Leu	Phe	Gln		
319				85					90					95			
321	tgc	ccg	tcc	ccg	gtt	tgg	gac	tcg	aag	ctc	ttc	aca	tgg	acc	gcc	aag	336
322	Cys	Pro	Ser	Pro	Val	Trp	Asp	Ser	Lys	Leu	Phe	Thr	Trp	Thr	Ala	Lys	
323				100					105					110			
325	gca	ttc	tat	tac	tcc	aag	tac	gtg	gag	tac	ctc	gac	acg	gcc	tgg	ctg	384
326	Ala	Phe	Tyr	Ser	Lys	Tyr	Val	Glu	Tyr	Leu	Asp	Thr	Ala	Trp	Leu		
327				115					120					125			
329	agg	gtc	tcc	ttt	ctc	cag	gcc	ttc	cac	cac	ttt	ggc	gcg	ccg	tgg	gat	432
330	Arg	Val	Ser	Phe	Leu	Gln	Ala	Phe	His	His	Phe	Gly	Ala	Pro	Trp	Asp	
331				130					135					140			
333	gtg	tac	ctc	ggc	att	cgg	ctg	cac	aac	gag	ggc	gta	tgg	atc	ttc	atg	480
334	Val	Tyr	Leu	Gly	Ile	Arg	Leu	His	Asn	Glu	Gly	Val	Trp	Ile	Phe	Met	
335	145								150					155			160
337	ttt	ttc	aac	tcg	ttc	att	cac	acc	atc	atg	tac	acc	tac	tac	ggc	ctc	528
338	Phe	Phe	Asn	Ser	Phe	Ile	His	Thr	Ile	Met	Tyr	Thr	Tyr	Tyr	Gly	Leu	
339				165						170				175			
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349	aac	gtc	ccc	tgc	ttc	aac	tcg	gac	aaa	ggg	aag	ttg	ttc	agc	tgg	gct	672
350	Asn	Val	Pro	Cys	Phe	Asn	Ser	Asp	Lys	Gly	Lys	Leu	Phe	Ser	Trp	Ala	
351				210					215					220			
353	ttc	aac	tat	gca	tac	gtc	ggc	tcg	gtc	ttc	ttg	ctc	ttc	tgc	cac	ttt	720
354	Phe	Asn	Tyr	Ala	Tyr	Val	Gly	Ser	Val	Phe	Leu	Leu	Phe	Cys	His	Phe	
355	225								230					235			240
357	ttc	tac	cag	gac	aac	ttg	gca	acg	aag	aaa	tcg	gcc	aag	gcg	ggc	aag	768
358	Phe	Tyr	Gln	Asp	Asn	Leu	Ala	Thr	Lys	Lys	Ser	Ala	Lys	Ala	Gly	Lys	
359					245					250					255		
361	cag	ctc	tag														777

<210> SEQ ID NO 115
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Unknown
 <220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(13)

<223> OTHER INFORMATION: Xaa in the sequence at position 2, 3, 4, 6, 7, 8 and 9
 has the meaning given in Table A.

<220> FEATURE:
 <221> NAME/KEY: MISC_FEATURE
 <222> LOCATION: (1)..(13)
 <223> OTHER INFORMATION: Consensus
 <400> SEQUENCE: 115

Asn Xaa Xaa Xaa His Xaa Xaa Met Tyr Xaa Tyr Tyr Xaa
 1 5 10

Tyr at this
 location

Invalid Response. 'Xaa' Represents
 Single Amino Acid. P/s see Item
 #9 in Error
 Summary Sheet.

F41

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/566,944

DATE: 02/14/2006
TIME: 12:55:18

Input Set : F:\Sequence listing (12810-00193-US).txt
Output Set: N:\CRF4\02142006\J566944.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:115; Xaa Pos. 2,3,4,6,7,10,13
Seq#:116; Xaa Pos. 3,4,5,6
Seq#:139; Xaa Pos. 3,4
Seq#:140; Xaa Pos. 2,3,5,6
Seq#:141; Xaa Pos. 3
Seq#:142; Xaa Pos. 5,6
Seq#:185; N Pos. 3,18
Seq#:186; N Pos. 3,9,12,15,21

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:115; Line(s) 12392
Seq#:116; Line(s) 12415
Seq#:140; Line(s) 13593
Seq#:142; Line(s) 13635

VERIFICATION SUMMARY

DATE: 02/14/2006

PATENT APPLICATION: US/10/566,944

TIME: 12:55:18

Input Set : F:\Sequence listing (12810-00193-US).txt

Output Set: N:\CRF4\02142006\J566944.raw

L:20 M:270 C: Current Application Number differs, Replaced Current Application No
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:12403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115 after pos.:0
L:12426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:116 after pos.:0
L:13581 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:139 after pos.:0
L:13602 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:140 after pos.:0
L:13623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:141 after pos.:0
L:13646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:142 after pos.:0
L:14407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:185 after pos.:0
L:14426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:186 after pos.:0